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Result
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Retinoblastoma bin
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## ALIGNMENTS

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Chen H,
                                                                                                                                                    mutation
                                                                                                                                                              Key
                                                                                                                                                                               Homo sapiens.
Synthetic.
                                                                                                                                                                                                        TIGR: trabecular meshwork induced glucocorticoid response protein; human: diagnosis; glaucoma; polymorphism; steroid sensitivity; mutant; ss.
                                                                                                                                                                                                                                   Human TIGR promoter mutant TIGRmt3 DNA.
                                                                                                                                                                                                                                                    27-OCT-1998 (first entry)
                                                                                                                                                                                                                                                                       V51364;
                                                                                                                                                                                                                                                                                       V51364 standard; DNA; 5304 BP
WPI; 1998-427946/36.
                                 (REGC ) UNIV CALIFORNIA.
                                                    26-SEP-1997;
28-JAN-1997;
                                                                               09-JAN-1998;
                                                                                                30-JUL-1998.
                                                                                                                 WO9832850-A1
                Chen P, Nguyen TD,
                                                    97US-0938669
97US-0791154
                                                                               98WO-US00468
                                                                                                                                                    Location/Qualifiers 4997..5002
                                                                                                                                /*tag= a
/note= "Wild-type TG is replaced with TGTGTG"
                 Polansky JR;
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Query Match
Best Local Similarity
Matches 5299; Conserv
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This sequence is a trabecular meshwork induced glucocorticoid response protein (TIGR) promoter mutant, TIGRmt4, which is used in a method for diagnosing glaucoma in a patient. The method involves the detection of polymorphisms whose presence is predictive of a mutation affecting TIGR response in the patient and can be diagnostic of glaucoma or steroid sensitivity. Base substitutions and base additions upstream of and within TIGR exons can also be used to diagnose glaucoma.
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27-OCT-1998 (first entry)

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TIGR; trabecular meshwork induced glucocorticoid response prote: diagnosis; glaucoma; polymorphism; steroid sensitivity; mutant; ss :ut

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Matches 5293; Conserv
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ssis; glaucoma; polymorphism; steroid sensitivity;
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Best Local s
Matches 222
                                                                                                                                                                                                                                                                                     detect insertions or deletions in DNA sequences. Such mutations markers of cancer so such primers can be used in the diagnosis of cancer, esp. colorectal, stomach or pancreatic tumours. See also Q63837-63.
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Query Match
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Matches 210;
                                                                                                    This sequence represents the retinoblastoma binding protein-7 (RBP-7) genomic sequence of the invention. The RBP-7 coding sequence and regulatory sequences are useful for the recombinant production of the protein and for expressing heterologous nucleic acids. Primers and probes derived from the RBP-7 nucleotide sequence (e.g. 287035-287099) are useful for DNA amplification and detection methods. RBP-7 bialielic markers (see 28693-287034) are useful for diagnosis of disease related to alteration in the regulation or in the coding regions of the RBP-7 gene and for prognosis/diagnosis of an eventual treatment with therapeutic agents, especially agents acting on pathologies involving abnormal cell proliferation and/or differentiation, these include thyroid hyperplasia, psoriasis, benign prostate hypertrophy, cancer, including breast cancer, sarcomas and other neoplasms, bladder cancer, colon cancer, lung cancer, prostate cancer, various leukaemias, and
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                                                                                                                                                                                                                                                                                                          Claim 1; Page 118-163; 223pp;
                                                                                                                                                                                                                                                                                                                                    differentiation -
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diagnosis; therapy; cell differentiation; thyroid hyperplasia; psoriasis;
benign prostate hypertrophy; cancer; sarcoma; neoplasm; leukaemia;
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Score 175.2;
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RESULT 14
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The invention relates to the amplification of region of DNA containing interspersed repetitive elements (IRE) such as the Alu repeat sequence presented here. The method involves ligating a double stranded DNA structure with a non-complementary region, a 'bubble', in the
                                                                                                                                                                                                                                                                                                                                                                                           Bubble; interspersed repetitive PCR; polymerase chain reaction; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-JUN-1997
                                                                       Amplification of nucleic acid having using bubble oligo:nucleotide
                                                                                                      WPI; 1997-108321/10.
                                                                                                                                                                 07-OCT-1993;
                                                                                                                                                                                     07-OCT-1993;
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                                                    Column 19-20;
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216..236
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                                                    16pp; English
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amplification; chromosomal aberration;
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                                                                                  interspersed repetitive
                                                                                                                                                                                                                                                  Alu-end
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                                                                                                                                                                                                                                                                                                                       (T62347)"
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                                                                                   element
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Best Local S
Matches 218
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TATA-box;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   containing IREs. The ligation results in a double stranded DNA molecule containing at least one 'bubble' at either end. After denaturing the structure, amplification of the IRE-containing region proceeds by PCR using primers targeted to the IRE sequence (e.g. see T62347-50) and to the sequence in the 'bubble' region (e.g. see T62345). The method can be used to detect the presence or absence of a chromosomal aberration e.g. in a genetic disorder, in a test organism.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q44278 standard;
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                                                                                         promoter
                                                                                                                                                                                                                                                                                                   misc_signal
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                                                                                                                                                             enhancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                218;
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                                                                                                                                                             514..541
                                                                                                                                                                                                                                                                                                     Location/Qualifiers 373..621
                                   /note= "eukaryotic promoter element;
claim 16 and 19-20, page 80"
                                                                                         582..602
                                                                                                      DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63 A; 75 C;
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78.7%;
                                                                                                                                                                                                                                                                                                                                                                                                             promoter; constitutive suppressor;
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                                                                                                                                                                                                                                                 '5' regulatory region; claim 1-3, page 78"
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; Pred. No. 9.1e
4; Mismatches
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Query Match
Best Local Similarity
Matches 227; Conserv
                                                                                                                                                                                                                                                                                                            A negative transcription regulatory element (a constitutive suppressor) between residues -250 and -190 (see tag b) of the 5' flanking region of the human serglycin gene, a positive (hematopoietic cell enhancer) regulatory element located between residues -118 and -81 (see tag c), an equiv. of the TATA-box and a novel eukaryotic promoter that utilises such equiv. (see tag d) are identified. The regulatory elements, vectors and hosts provided with these elements, are useful in the control of gene transcription of heterologous genes in eukaryotic cells, esp. hematopoietic cells.
                                                                                                                                         1321 acctgagctcactgccacctctgcctcccaggttcaagcaattctcctgtctcagcctcc 1380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transcription regulatory elements of ser-glycin gene - spec for haematopoietic cells, also trans-acting transcriptional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-JAN-1992;
02-JUL-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_difference
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                                                                                                                                                                                                                                                                                 Sequence 17327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 4B-J; 112pp; English.
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                                                                     cgcgtagctgggactacaggcgcacgc-----ccggctaatttttgtattgttagta 1432
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DB; R39393.
gagatggggfttcaccatattagcccggctggtcttgaactcctgacctcaggtgatcca
                                                     CGAGTAGCTGGGATGACAGGTGCCCACAATCATATCCAGCTAATTTTTGTATTTTAGTA
                                                                                                                        ATCTCGGCTCACTGCAACCTCTGCCTCCCAGGTTCAAGCGATTCTCCTGCCTCAGCCTCC
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9597..9744
                                                                                                                                                                                                                                                                                  BP; 4936 A;
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92US-0906871.
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6135
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675..9598
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622..753
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/number= ;
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attachment region"
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Pred.
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No. 6.9
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                                                                                                                                                                                               Query Match 3.3%;
Best Local Similarity 81.0%;
Matches 217; Conservative
                                                                                                                                                                                                                                                                                                                                                                This invention describes novel nucleic acids (I; designated LOBO (long bones)) encoding proteins influencing bone development in mammals. The proteins of the invention reduce and/or inactivate bone extension (i.e. development), with exception of the skull and have osteopathic activity. The nucleic acid molecules, proteins and antibodies can be used in diagnostic or pharmaceutical compounds e.g. for gene therapy. The methods and nucleic acid molecules, etc. are useful for production of transgenic animals, especially a transgenic mouse for the study of diseases associated with bone development, e.g. spondyloepiphysal dysplasia and achondroplasia. This sequence encodes a human LOBO protein described in the method of the invention.
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                                                   1380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-JAN-2000
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                                                                                             CCCGCCTCAGTCTCCCAAAGTGCTGGGATTACAGGTGTGAGCCACCACCACCCGCCGAAA 7527
                         ccgcgtagctgggactacaggcg-----cacgcccggctaattttttgtatttgttagt 1431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTACTTTTATGGAAAAGACAATGTGGCATTGTAGAAAAACCTATACTTAAAAA
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ccgagtagctgggattacaagtgcccgccaccacgcccagctaatttttgtattttagt 4110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard;
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 Page 244-271;

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                                                                                                                                                                                                                                                                                                                         BP; 11432
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                                                                                                                                                                                                                                                                                                                         A; 13017 C;
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                                                                                                                                                                                               Score 173.2; Pred. No. 1.3e 0; Mismatches
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                                                                                                                           01-MAY-1995;
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genomic locus; gene mapping; paternity;
forensic science; fingerprinting; ss.
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                Example 1; Fig 1; 23pp;
                                          DNA amplification primer pair - of multiple highly polymorphic of
                                                                      WPI; 1996-506179/50.
                                                                                        Labuda
                                                                                                                                             01-MAY-1996;
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                                                                                                                                                                                                  "sequence contains between 3 nucleotides in this region"
                                                                                                                                                                                                                                                                 "repeated 7-12 times; this sequence repeats of this sequence"
                                                                                                                                                                                                                                                                                                                                                        "sequence contains between nucleotides in this region
                                                                                                                                                                                                                                                                                                 "this specification discloses that the repeat unit
TAAA (bases 27-30; see below) is repeated 7-12
times; this sequence contains 12 repeats of the
TAAA sequence"
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                                           for simultaneous amplification ic loci, partic. for
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maternity; children;
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locus
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Q560
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                                                                                                                                                                                                             amplified by the primer pair R14B264/Q560mak (T42806-7). The primers also simultaneously amplify the loci Q900 (T42808) and Q120 (T42810). The primers can be used for gene mapping, to assess paternity, maternity and identity of children or in forensic science. In particular, they can be used for the DNA fingerprinting identification of genetically related or unrelated individuals.
1381 cgcgtagctgggactacaggcg------cacgcccggctaatttttgtattgttagta 1432
                                                                                                                                                                                                                                                                                                                                                                          Sequence 452 BP; 149 A; 92 C; 106 G; 85 T; 20 other;
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